

*F. Harad*

## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH

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OCT 17 2000

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/265,540B

Source: 1643

Date Processed by STIC: 10/2/2000

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

F. HARVUD

1643

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/265,540B

DATE: 10/02/2000  
 TIME: 10:47:24

Input Set : A:\804Krvs2.txt  
 Output Set: N:\CRF3\09292000\I265540B.raw

Does Not Comply  
 Corrected Diskette Needed

3 <110> APPLICANT: Parham, Christi L.  
 4       Moore, Kevin W.  
 5       Murgolo, Nicholas J.  
 6       Bazan, J. Fernando

8 <120> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods

10 <130> FILE REFERENCE: DX0804

12 <140> CURRENT APPLICATION NUMBER: US/09/265,540B

13 <141> CURRENT FILING DATE: 1999-03-08

15 <160> NUMBER OF SEQ ID NOS: 6

17 <170> SOFTWARE: PatentIn Ver. 2.0

19 <210> SEQ ID NO: 1

20 <211> LENGTH: 1381

21 <212> TYPE: DNA

22 <213> ORGANISM: primate

24 <220> FEATURE:

25 <221> NAME/KEY: CDS

26 <222> LOCATION: (132)..(1064)

28 <220> FEATURE:

29 <221> NAME/KEY: misc\_feature

30 <222> LOCATION: n at position 567 and 573

31 <223> OTHER INFORMATION: n may be A, C, T, or G; translated amino acid depends on genetic code

33 <400> SEQUENCE: 1

34 tcgaccacg cgtccgcgtc gcgactcaga cctcagtc aacatatgc ttctgaagaa 60

36 agatggctga gatggacaga atgcattttt ttggaaagaa acaatgttct aggtcaaact 120

38 gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170

39                   Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr

40                   1               5               10

42 agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca 218

43 Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr

44                   15               20               25

46 gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca 266

47 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser

48                   30               35               40               45

50 acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga 314

51 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly

52                   50               55               60

54 gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg 362

55 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu

56                   65               70               75

58 tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa 410

59 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu

60                   80               85               90

62 ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac 458

63 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr

64                   95               100               105

66 aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc 506

67 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser

f.2

what about n's at positions 1336, 1342, or  
 1369?

(P.2)

**RAW SEQUENCE LISTING**

PATENT APPLICATION: US/09/265,540B

DATE: 10/02/2000

TIME: 10:47:24

Input Set : A:\804Krvs2.txt

Output Set: N:\CRF3\09292000\I265540B.raw

68	110	115	120	125
70	atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct			554
71	Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro			
72	130	135	140	
74	ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag			602
75	Gly Met Glu Ile Xaa Ly <del>s</del> Xaa Gly Phe His Leu Val Ile Glu Leu Glu			
76	145	150	155	
78	gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag			650
79	Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu			
80	160	165	170	
82	cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca			698
83	Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro			
84	175	180	185	
86	gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc			746
87	Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala			
88	190	195	200	205
90	cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca			794
91	Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr			
92	210	215	220	
94	gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg			842
95	Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu			
96	225	230	235	
98	ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc			890
99	Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe			
100	240	245	250	
102	gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg			938
103	Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val			
104	255	260	265	
106	gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc			986
107	Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile			
108	270	275	280	285
110	agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct			1034
111	Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser			
112	290	295	300	
114	cct gag gaa ctc ctc agg gcc tgg atc tca taggttgcg gaaggccca			1084
115	Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser			
116	305	310		
118	ggtaagccg agaacctgg tctcatgaca tggaaaccat gaggggacaa gtttgtttc			1144
120	tgtttcccg cacggacaaag ggatgagaga agtaggaaga gcctgtgtc tacaagtcta			1204
122	gaagcaacca tcagaggcg ggtgtttgt ckaacagaac aaytgactga ggytakrggg			1264
124	gtwtgtgactt cttagacttg ggstksayt tgwtggtyt agcaaccctg gaaaaagtga			1324
126	cttcatccct tnggtccaa gtttctcat ctgtaatggg ggtatctac aaaactg			1381
129	<210> SEQ_ID NO: 2			
130	<211> LENGTH: 311			
131	<212> TYPE: PRT			
132	<213> ORGANISM: primate			
134	<220> FEATURE:			
135	<221> NAME/KEY: misc_feature / / / / /			
136	<222> LOCATION: Xaa at residues 146, 148, 171, 214 and 225			

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,540B

DATE: 10/02/2000

TIME: 10:47:24

Input Set : A:\804Krvs2.txt

Output Set: N:\CRF3\09292000\I265540B.raw

137 <223> OTHER INFORMATION: Xaa depends on corresponding codon  
 139 <400> SEQUENCE: 2  
 140 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe  
 141 1 5 10 15  
 143 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val  
 144 20 25 30  
 146 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met  
 147 35 40 45  
 149 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val  
 150 50 55 60  
 152 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser  
 153 65 70 75 80  
 155 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu  
 156 85 90 95  
 158 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg  
 159 100 105 110  
 161 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys  
 162 115 120 125  
 164 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu  
 165 130 135 140  
 W--> 167 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly  
 168 145 150 155 160  
 W--> 170 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala  
 171 165 170 175  
 173 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu  
 174 180 185 190  
 176 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe  
 177 195 200 205  
 W--> 179 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val  
 180 210 215 220  
 W--> 182 Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe  
 183 225 230 235 240  
 185 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys  
 186 245 250 255  
 188 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro  
 189 260 265 270  
 191 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg  
 192 275 280 285  
 194 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu  
 195 290 295 300  
 197 Leu Leu Arg Ala Trp Ile Ser  
 198 305 310  
 201 <210> SEQ ID NO: 3  
 202 <211> LENGTH: 1244  
 203 <212> TYPE: DNA  
 204 <213> ORGANISM: primate  
 206 <220> FEATURE:  
 207 <221> NAME/KEY: CDS  
 208 <222> LOCATION: (2)..(694)

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,540B

DATE: 10/02/2000

TIME: 10:47:24

Input Set : A:\804Krvs2.txt  
 Output Set: N:\CRF3\09292000\I265540B.raw

210 <400> SEQUENCE: 3  
 211 c cgg gtc gac cca cgc gtc cgc ctg gtt tcc ccc tgg ctg aca gtg cct 49  
 212 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro  
 213 1 5 10 15  
 215 tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc 97  
 216 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile  
 217 20 25 30  
 219 tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc 145  
 220 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro  
 221 35 40 45  
 223 ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay 193  
~~OP~~  
 224 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa  
 225 50 55 60  
 227 tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac 241  
 228 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn  
 229 65 70 75 80  
 231 tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa 289  
 232 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln  
 233 85 90 95  
 235 gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc acc tct agg ccc ggc 337  
 236 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly  
 237 100 105 110  
 239 cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg 385  
 240 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr  
 241 115 120 125  
 243 aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg 433  
 244 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu  
 245 130 135 140  
 247 gcg gcg ctg gcg ggg ggc tgt ttc ctg gtg ctg aga tac aaa ggc 481  
 248 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly  
 249 145 150 155 160  
 251 ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc 529  
 252 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile  
 253 165 170 175  
 255 gaa gag tat ctg aag gac ccc agc cag cct atc cta gag gcc ctg gac 577  
 256 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp  
 257 180 185 190  
 259 aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt 625  
 260 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val  
 261 195 200 205  
 263 gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc 673  
 264 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr  
 265 210 215 220  
 267 caa aac tct ggt gcg gtc tagcctgtgg ggtaagggtt ctgagccgag 724  
 268 Gln Asn Ser Gly Ala Val Cys  
 269 225 230  
 271 gaagctgctg atgtccatgt cagcacatcta tggaatccgg tcctccatcc tcctgtcccc 784  
 273 aaaaggcccg tcagtgcctg tgaagatgtt acgggtctca tgggggcgac aagcttattt 844  
 275 atttttttct tcaaactaag agttttctaa tcatacgcgt ttttagaata attctacaga 904

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/265,540BDATE: 10/02/2000  
TIME: 10:47:24Input Set : A:\804Krvs2.txt  
Output Set: N:\CRF3\09292000\I265540B.raw

277 tatgtccccc aaagattnaa atttctctta aacactaaaa agacatgtaa ttatttggta 964  
 279 gcaaatgggc gtctggcaca cctctgacac ttttcgtca gcagccagga cacgaggctc 1024  
 281 cctcttgat gaagccccctc gggcagacca tgtcacctgt cccagcctgc cccaagaagg 1084  
 283 gacattaagt ggccttctt catatccaaa cacctggctt gaaatgtgtat tagccctgtt 1144  
 285 aatagtttca cagagattnaa gcctttttt cccccaagt aggaataaaa gactataatt 1204  
 287 aacttttaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1244  
 290 <210> SEQ ID NO: 4  
 291 <211> LENGTH: 231  
 292 <212> TYPE: PRT  
 293 <213> ORGANISM: primate  
 295 <220> FEATURE:  
 296 <221> NAME/KEY: misc\_feature  
 297 <222> LOCATION: Xaa at residue 64  
 298 <223> OTHER INFORMATION: Xaa translated amino acid depends on corresponding codon  
 300 <400> SEQUENCE: 4  
 301 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro  
 302 1 5 10 15  
 304 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile  
 305 20 25 30  
 307 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro  
 308 35 40 45  
 310 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa  
 311 50 55 60  
 313 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn  
 314 65 70 75 80  
 316 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln  
 317 85 90 95  
 319 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly  
 320 100 105 110  
 322 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr  
 323 115 120 125  
 325 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu  
 326 130 135 140  
 328 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly  
 329 145 150 155 160  
 331 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile  
 332 165 170 175  
 334 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp  
 335 180 185 190  
 337 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val  
 338 195 200 205  
 340 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr  
 341 210 215 220  
 343 Gln Asn Ser Gly Ala Val Cys  
 344 225 230  
 347 <210> SEQ ID NO: 5  
 348 <211> LENGTH: 337  
 349 <212> TYPE: PRT  
 350 <213> ORGANISM: primate

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/265,540B

DATE: 10/02/2000

TIME: 10:47:25

Input Set : A:\804Krvs2.txt  
Output Set: N:\CRF3\09292000\I265540B.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:224 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
L:224 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3  
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821-1.825 for the following reason(s):



1. This application clearly fails to comply with the requirements of 37 CFR 1.821-1.825. Applicant's attention is directed to these regulations, published at 114 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.



2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).



3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).



4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of marked-up "Raw Sequence Listing."



5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).



6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).



7. Other: \_\_\_\_\_

**Applicant must provide:**



- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"



- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification



- A statement that the content of the paper and computer readable copies are the same, and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.